OIPE

RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/029,359   TIME: 07:45:59

Input Set : A:\10806156.txt
Output Set: N:\CRF3\01152002\J029359.raw

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 3 <110>  APPLICANT: Pharmacia AB
 5 <120>  TITLE OF INVENTION: Protein Cluster II
 7 <130>  FILE REFERENCE: 00404
 9 <140>  CURRENT APPLICATION NUMBER: US/10/029,359
 9 <141>  CURRENT FILING DATE: 2001-12-21
 9 <160>  NUMBER OF SEQ ID NOS: 6
11 <170>  SOFTWARE: PatentIn version 3.0
13 <210>  SEQ ID NO: 1
14 <211>  LENGTH: 505
15 <212>  TYPE: DNA
16 <213>  ORGANISM: human
18 <220>  FEATURE:
19 <221>  NAME/KEY: CDS
20 <222>  LOCATION: (21)..(497)
22 <220>  FEATURE:
23 <221>  NAME/KEY: misc_feature
24 <222>  LOCATION: (297)..()
25 <223>  OTHER INFORMATION: n=a, g, c or t
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29                      Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser
30                       1               5                  10
32 aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg  101
33 Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly
34             15                  20                  25
36 ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt  149
37 Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly
38         30                  35                  40
40 gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca  197
41 Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser
42     45                  50                  55
44 gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca  245
45 Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala
46 60                  65                  70                  75
48 gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc  293
49 Asp Ser Ser Gln Arg Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu
50                  80                  85                  90
52 tat nag caa gtt aaa att ctt tgc tgg gtt atg aca ggc tct caa aac  341
53 Tyr Xaa Gln Val Lys Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn
54             95                  100                 105
56 cta cag aaa aag gcc aaa cat gtc aaa gct aca tgg gcc cag cgt tgt  389
57 Leu Gln Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys
58         110                 115                 120
60 cta aaa gta ttt ttt atg agt tca gaa gaa aat aaa gac ttc cgt gct  437
61 Leu Lys Val Phe Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala
62     125                 130                 135
64 gtg gga ttg aaa acc aaa gca ggc aga gat gag cta tac tgg aaa aca  485
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65 Val Gly Leu Lys Thr Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr
66 140               145               150               155
68 att aac ctt ttc agtatgtt                                           505
69 Ile Asn Leu Phe
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 159
75 <212> TYPE: PRT
76 <213> ORGANISM: human
78 <220> FEATURE:
79 <221> NAME/KEY: misc_feature
80 <222> LOCATION: (297)..()
81 <223> OTHER INFORMATION: n=a, g, c or t
83 <400> SEQUENCE: 2
85 Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser Lys Ser Trp Leu Asn
86 1               5               10               15
89 Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly Phe Ile Leu Phe Ser
90                 20              25              30
93 Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
94             35              40              45
97 Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
98     50              55              60
101 Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
102 65              70              75              80
```
W-->
```
105 Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr Xaa Gln Val Lys
106               85              90              95
109 Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn Leu Gln Lys Lys Ala
110               100             105             110
113 Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Leu Lys Val Phe Phe
114         115             120             125
117 Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala Val Gly Leu Lys Thr
118     130             135             140
121 Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr Ile Asn Leu Phe
122 145             150             155
125 <210> SEQ ID NO: 3
126 <211> LENGTH: 489
127 <212> TYPE: DNA
128 <213> ORGANISM: human
130 <220> FEATURE:
131 <221> NAME/KEY: CDS
132 <222> LOCATION: (55)..(489)
134 <400> SEQUENCE: 3
136 catctaaaaa gactgatgaa gttgattgca aatgctagtc atcataaata ccag aac     57
137                                                              Asn
138                                                              1
140 aca ggt gtc act gac aaa ctc tat caa aag atg aaa att ctt tgc tgg   105
141 Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp
142             5               10              15
144 att atg aca gga cct caa aat cta gaa aaa aag atc aga cgc atc aga   153
145 Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg
```

[handwritten annotation: This is an amino acid sequence. Xaa is at location 93.]

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146          20                    25                    30
148 gat aca tgg gcc cag ggt tgc aat aaa gcg ttg ttt atg agc tca aaa     201
149 Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser Lys
150      35                    40                    45
152 gaa aat aaa gac ttc tct act gtg gga tta cac acc aaa gaa gac aga     249
153 Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp Arg
154 50                    55                    60                    65
156 aac caa ctg tcc tgg aaa ata gtt aaa gct ttt cta tat gct cat gac     297
157 Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp
158                    70                    75                    80
160 cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata     345
161 His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile
162                85                    90                    95
164 tgt ata tat atc aca ttg gac aac ttg aaa tgg ctt ctc aca aac tat     393
165 Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr
166          100                   105                   110
168 aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga     441
169 Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg
170      115                   120                   125
172 aaa cag gac tac atg act gga gga gca gga tat gta ctg agc aaa gaa     489
173 Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu
174 130                   135                   140                   145
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177 <210> SEQ ID NO: 4
178 <211> LENGTH: 145
179 <212> TYPE: PRT
180 <213> ORGANISM: human

182 <400> SEQUENCE: 4

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184 Asn Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys
185 1               5                   10                  15
188 Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
189             20                    25                    30
192 Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
193         35                    40                    45
196 Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
197     50                    55                    60
200 Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
201 65                    70                    75                    80
204 Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
205                   85                    90                    95
208 Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
209             100                   105                   110
212 Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
213         115                   120                   125
216 Arg Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys
217     130                   135                   140
220 Glu
221 145
```

224 <210> SEQ ID NO: 5
225 <211> LENGTH: 1560

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226 <212> TYPE: DNA
227 <213> ORGANISM: human
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (2)..(934)
233 <400> SEQUENCE: 5
234 a gat aat gga cag aat cat cta gaa gga caa atg aac ttc aat gca gat        49
235   Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
236   1               5                   10                  15
238 tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat        97
239 Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
240            20                  25                  30
242 cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta       145
243 Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
244        35                  40                  45
246 gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac       193
247 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
248    50                  55                  60
250 aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg       241
251 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
252 65                  70                  75                  80
254 gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att       289
255 Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
256                85                  90                  95
258 aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg       337
259 Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
260            100                 105                 110
262 ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg       385
263 Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
264        115                 120                 125
266 tgg ctt ctt tca aaa tac gac cct gaa gaa ccc att tac ttt ggg aga       433
267 Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
268    130                 135                 140
270 aga ttt aag cct tat gta aag cag ggc tac atg agt gga gga gca gga       481
271 Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
272 145                 150                 155                 160
274 tat gta cta agc aaa gaa gcc ttg aaa aga ttt gtt gat gca ttt aaa       529
275 Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
276                165                 170                 175
278 aca gac aag tgt aca cat agt tcc tcc att gaa gac tta gca ctg ggg       577
279 Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
280            180                 185                 190
282 aga tgc atg gaa att atg aat gta gaa gca gga gat tcc aga gat acc       625
283 Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
284        195                 200                 205
286 att gga aaa gaa act ttt cat ccc ttt gtg cca gaa cac cat tta att       673
287 Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
288    210                 215                 220
290 aaa ggt tat cta cct aga acg ttt tgg tac tgg aat tac aac tat tat       721
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291 Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
292 225                 230                 235                 240
294 cct cct gta gag ggt cct ggt tgc tgc tct gat ctt gca gtt tct ttt      769
295 Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
296             245                 250                 255
298 cac tat gtt gat tct aca acc atg tat gag tta gaa tac ctc gtt tat      817
299 His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
300             260                 265                 270
302 cat ctt cgt cca tat ggt tat tta tac aga tat caa cct acc tta cct      865
303 His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
304         275                 280                 285
306 gaa cgt ata cta aag gaa att agt caa gca aac aaa aat gaa gat aca      913
307 Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
308         290                 295                 300
310 aaa gtg aag tta gga aat cct tgaaagaaaa tcatgaatga acaaaggtaa         964
311 Lys Val Lys Leu Gly Asn Pro
312 305                 310
314 tatgtctagc actgcactga aaaaggactt ctgcatttct gacatagaac actggaatcc    1024
316 cagtgaggaa ttctaagtga acattcctta tagaaacctt tcacatgaat gactataaac    1084
318 tgaagcttta aatgagctgt gaagtgtgtt aaaatgtgtt ttgatacagt aatatataaa    1144
320 tatgtctata tatatgagga acttgtgttt tttaaatggt ggccaggtag aggaactaga    1204
322 aaagagattt tgttgcctgt tttctgacca tctgtgttat tgtcactgag aaactaaaat    1264
324 agtaaattta ctaaaactac actgcaccat gttagtaata aacagatctg ccttaaagaa    1324
326 aagaaaattt tagaaagaaa tattgttgct cagtgttgtt aatatagctc aagaattgag    1384
328 tttatatttg cagtatgcta taaatgatac cccctacca cacccacaca cacagttttt     1444
330 gtctaatgaa aatgttgctg tgattatta taattggtag tatttcttcc agaagaagct      1504
332 aaaataagac tggcacttac cctgaagtgc attaataaaa ccacacttta aaatta        1560
335 <210> SEQ ID NO: 6
336 <211> LENGTH: 311
337 <212> TYPE: PRT
338 <213> ORGANISM: human
340 <400> SEQUENCE: 6
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342 1                 5                 10                 15
345 Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
346             20                 25                 30
349 Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
350             35                 40                 45
353 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
354         50                 55                 60
357 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
358 65                 70                 75                 80
361 Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
362             85                 90                 95
365 Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
366             100                 105                 110
369 Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
370         115                 120                 125
373 Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
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VERIFICATION SUMMARY   DATE: 01/15/2002
PATENT APPLICATION: US/10/029,359   TIME: 07:46:00

      Input Set : **A:\10806156.txt**
      Output Set: **N:\CRF3\01152002\J029359.raw**

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
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